



2857

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE  
PATENT TRANSMITTAL FORM

Applicant(s): John R. Desjarlais

Serial No.: 09/877,695

For: APPARATUS AND METHOD FOR DESIGNING PROTEINS AND PROTEIN  
LIBRARIES

Filed: June 8, 2001

Examiner: Not Yet Assigned

Art Unit: 2857

Attorney Docket: 823.0093USU

COMMISSIONER FOR PATENTS  
Washington, D.C. 20231

Sir:

Transmitted herewith is:

1. Information Disclosure Statement;
2. PTO Form 1449 with copies of patents;
3. Transmittal letter in duplicate; and
4. Postcard.

Please charge any additional fees or credit any such fees, if necessary to Deposit Account No. 01-0467 in the name of Ohlandt, Greeley, Ruggiero & Perle. A duplicate copy of this sheet is attached.

Respectfully submitted,

Date: December 28, 2001

Paul D. Greeley, Esq.  
Reg. No. 31,019  
Ohlandt, Greeley, Ruggiero & Perle, L.L.P.  
One Landmark Square, 10th Floor  
Stamford, Connecticut 06901-2682  
(203) 327-4500

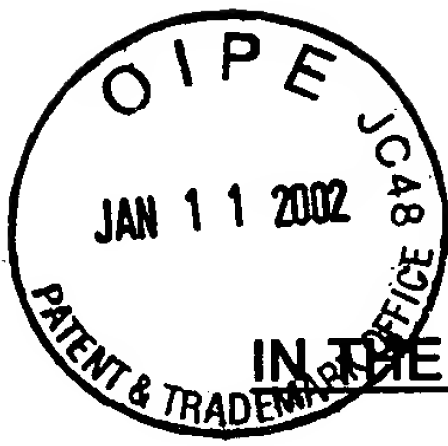
**CERTIFICATE OF MAILING**

I HEREBY CERTIFY THAT THIS CORRESPONDENCE IS BEING DEPOSITED WITH THE U.S. POSTAL SERVICE AS FIRST CLASS MAIL IN AN ENVELOPE ADDRESSED TO: COMMISSIONER FOR PATENTS, WASHINGTON, D.C. 20231, ON DECEMBER 28, 2001.

Jeffrey J. Scepanski  
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12/28/01  
DATE



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Plunkett  
2/20/03

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**INFORMATION DISCLOSURE STATEMENT**

Sir:

In accordance with applicant's duty of disclosure under 37 C.F.R. §1.56, please find attached hereto form PTO-1449 listing information which may be material to the patentability of this application. This Information Disclosure Statement is being filed:

\_\_\_ Within three (3) months of the filing date of the national application;

\_\_\_ Within three (3) months of the date of entry of the national stage as set forth in 37 C.F.R. §1.491 in an international application;

**XXX** Before the mailing date of a first Office Action on the merits;

\_\_\_ After the filing date or date of first Office Action, but before the mailing date of a final action under 37 C.F.R. §1.113, provided that this occurs prior to the issuance of a Notice of Allowance and provided that this I.D.S. is accompanied by either a certification as specified in 37 C.F.R. §1.97(e) or the fee set forth in 37 C.F.R. §1.17(p);

- \_\_\_\_\_ After the filing date or date of first Office Action, but before the mailing date of a Notice of Allowance under 37 C.F.R. §1.311, provided that this occurs prior to the final action and provided that this I.D.S. is accompanied by either a certification as specified in 37 C.F.R. §1.97(e) or the fee set forth in 37 C.F.R. §1.17(p);
- \_\_\_\_\_ After the mailing date of a final action under 37 C.F.R. §1.113, provided that this occurs prior to the issuance of a Notice of Allowance and provided that this I.D.S. is accompanied by either a certification as specified in 37 C.F.R. §1.97(e), a petition requesting consideration of the I.D.S., and the petition fee set forth in 37 C.F.R. §1.17(i)(1); and
- \_\_\_\_\_ After the mailing date of a Notice of Allowance under 37 C.F.R. §1.311, provided that this occurs prior to the issuance of a final action and provided that this I.D.S. is accompanied by either a certification as specified in 37 C.F.R. §1.97(e), a petition requesting consideration of the I.D.S., and the petition fee set forth in 37 C.F.R. §1.17(l)(1).

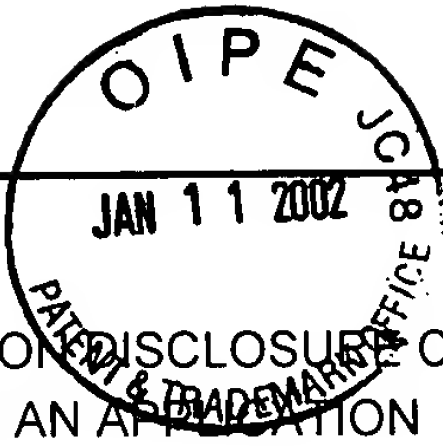
It should be understood that attention has been called to the references that have been deemed to be pertinent to the claimed present invention. In concluding what was pertinent, the criteria employed was considered most appropriate in light of the invention shown in the present application. However, the Examiner or others may deem some other criteria to be just as appropriate or more appropriate. Therefore, the Examiner is respectfully urged to review the listed references and to make the usual careful independent search for other prior art that may be pertinent.

Respectfully submitted,



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Reg. No. 31,019  
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(203) 327-4500

Sheet 1 of 13

FORM PTO-1449

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(Use several sheets if necessary)

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Applicant

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## U. S. PATENT DOCUMENTS

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## FOREIGN PATENT DOCUMENTS

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						YES	NO

## OTHER DOCUMENTS (including Author, Title, Date, Pertinent Pages, Etc.)

	Dahiyat et al. "Automated design of the surface positions of protein helices." <i>Protein Science</i> . (1997), 6: 1333-1337.
	Dahiyat et al. "Protein design automation." <i>Protein Science</i> . (1996), 5: 895-903.
	Dahiyat et al. "De novo protein design: Fully automated sequence selection." <i>Science</i> . Vol. 278, 3 Oct. 1997, 82-87.

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	Dahiyat et al. "Probing the role of packing specificity in protein design." <i>Proc. Natl. Acad. Sci. USA</i> . Vol. 94, 10172-10177, Sept. 1997.
	Dahiyat et al. "De novo protein design: Towards fully automated sequence selection." <i>J. Mol. Biol.</i> (1997) 273, 789-796.
	Delarue et al. "The inverse protein folding problem: Self consistent mean field optimisation of a structure specific mutation matrix." <i>Pac Symp Biocomput.</i> (1997), 109-121.

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	Desjarlais et al. "Computer Search Algorithms in protein modification and design." (1998) <i>Curr Opin Struct Biol.</i> 8(4), 471-5.
	Desjarlais et al. "De novo design of the hydrophobic cores of proteins." <i>Protein Science</i> (1995), 4, 2006-18.
	Desjarlais et al. "Side-chain and backbone flexibility in protein core design. <i>J. Mol. Biol.</i> (1999), 290(1), 305-18.

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	Desmet et al., "The dead-end elimination theorem and its use in protein side-chain positioning." <i>Nature</i> . (1992), 356(9), 539-542.
	Dunbrack et al. "Bayesian statistical analysis of protein side-chain rotamer preferences. <i>Protein Sci.</i> (1997), 6(8), 1661-81.
	Eisenberg et al., "Solvation energy in protein folding and binding." <i>Nature</i> . 319(6050), 199-203.

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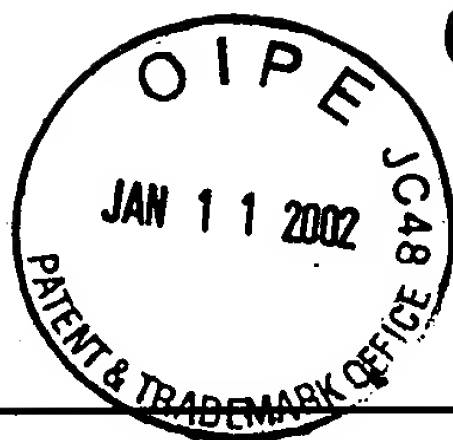
	Goldstein. "Efficient rotamer elimination applied to protein side-chains and related spin glasses. <i>Biophys. J.</i> (1994), 66(5), 1335-40.
	Gordon. "Energy functions for protein design. <i>Curr Opin Struct Biol.</i> (1999), 9(4), 509-13.
	Harbury et al. "Repacking protein cores with backbone freedom: structure prediction for coiled coils." <i>Proc Natl Acad Sci USA.</i> (1995), 92(18), 8408-12.

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	Hellinga. "Rational protein design: combining theory and experiment." <i>Proc Natl Acad Sci USA</i> . (1997), 94(19), 10015-17.
	Hellinga et al. "Optimal sequence selection in proteins of known structure by simulated evolution." <i>Proc Natl Acad Sci USA</i> . (1994), 91(13), 5803-7.
	Hendsch et al. "Electrostatic interactions in the GCN4 leucine zipper: Substantial contributions arise from intramolecular interactions enhanced on binding. <i>Protein. Sci.</i> (1999), 8(7), 1381-92.

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	Henikoff et al. "Position-based sequence weights. <i>J. Mol. Biol.</i> (1994), 243(4), 574-8.
	Holland. <i>Adaptation in natural and artificial systems</i> . The MIT Press, Cambridge, MA (1992).
	Johnson et al. "Solution structure and dynamics of a designed hydrophobic core variant of ubiquitin. <i>Structure Fold Des.</i> (1999), 7(8), 967-76.

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	Jorgensen et al. "The OPLS potential functions for proteins. Energy minimizations for crystals of cyclic peptides and crambin." <i>J. Amer. Chem. Soc.</i> (1988), 110(6), 1657-1666.
	Koehl et al. "Application of a self-consistent mean field theory to predict protein side-chains conformation and estimate their conformational entropy." <i>J. Mol. Biol.</i> , 239(2), 249-75.
	Koehl et al. "Mean-field minimization methods for biological macromolecules." <i>Curr Opin Struct Biol.</i> , (1996), 6(2), 222-6.

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	Kono et al. "Energy minimization method using automata network for sequence and side-chain conformation prediction from given backbone geometry." <i>Proteins</i> . (1994), 19(3), 244-255.
	Kono et al. "Designing the hydrophobic core of <i>Thermus flavus</i> malate dehydrogenase based on side-chain packing." <i>Protein Eng.</i> (1998), 11(1), 47-52.
	Kuhlman et al. "Native protein sequences are close to optimal for their structures." <i>Proc. Natl. Acad. Sci. USA</i> . (2000), 97(19), 10383-8.

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	Lazar et al. "De novo design of the hydrophobic core of ubiquitin." <i>Protein Sci.</i> (1997), 6(6), 1167-78.
	Lazar et al. "Rotamer strain as a determinant of protein structural specificity." <i>Protein Sci.</i> (1999), 8(12), 2598-610.
	Lee. "Predicting protein mutant energetics by self-consistent ensemble optimization." <i>J. Mol. Biol.</i> (1994), 236(3), 918-39.

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	Micheletti et al. "Design of proteins with hydrophobic and polar amino acids." <i>Proteins</i> . (1998), 32(1), 80-7.
	Raha et al. "Prediction of amino acid sequence from structure." <i>Protein Sci.</i> (2000), 9(6), 1106-19.
	Ranganathan et al. "Structural and functional analysis of the mitotic rotamase Pin1 suggests substrate recognition is phosphorylation dependent." <i>Cell</i> . (1997), 89(6), 875-86.

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	Street et al. "Computational protein design." <i>Structure Fold Des.</i> (1999), 7(5), R105-9.
	Su et al. "Coupling backbone flexibility and amino acid sequence selection in protein design." <i>Protein Sci.</i> (1997), 6(8), 1701-7.
	Voigt et al. "Trading accuracy for speed: A quantitative comparison of search algorithms in protein sequence design." <i>J. Mol. Biol.</i> (2000), 299(3), 789-803.

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	Voigt et al. "Computational method to reduce the search space for directed protein evolution." <i>Proc. Natl. Acad. Sci. USA.</i> (2001), 98(7), 3778-83.
	Weiner et al. "A new force field for molecular mechanical simulation of nucleic acids and proteins." <i>Journal of the American Chemical Society.</i> (1984), 106(3), 765-84.

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